



Amendments to the Specification:

Please replace the "Reference to Related Applications" section with the following amended paragraphs:

The present application includes the subject of Provisional Application Serial No. 60/455,563 filed March 19, 2003 and claims the priority thereof.

The present application is a continuation in part of US Patent Application Serial Number 09/866,925 filed May 30, 2001 entitled ALGORITHMIC DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES[[.]] (referred to as "basic methods patent application"); and claims the priority thereof.

This present application is related to PCT application PCT/US01/16471 filed May 31, 2001 and entitled ALGORITHMIC DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES.

The present application is also related to US Patent Application Serial Number 10/339,666 filed January 10, 2003 entitled SIMULATION OF GENE EXPRESSION CONTROL USING CONNECTRONS, INTERFERENCE RNAS (IRNAS) AND SMALL TEMPORAL RNAS (STRNAS) IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES

The present application is also related to US Patent Application Serial Number 10/364,516 filed February 12, 2003 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE ESCHERICHIA COLI K-12 MG1655 COMPLETE GENOME

The present application is also related to US Patent Application Serial Number 10/364,412 filed February 12, 2003 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE SACCHAROMYCES CEREVISIAE COMPLETE GENOME, ~~and applicant claims the priority of each of the above identified pending applications.~~

On page 3, please replace the two sections entitled "**Reverse Complement**" and "**Equivalent Sequences**" (at actual lines 3-15) with the following amended sections thereof:

Reverse Complement - Going away from a given point, the same sequence occurs on opposite strands. In the example below the sequence GCATCC in the dominant direction of the positive strand occurs somewhere else in the genome in the anti-dominant direction of the negative strand

Positive Strand
SEQ ID No. 121

5'- **GCATCC**GTGTAAT ATTACACGGATGC -3'

Negative Strand
SEQ ID No. 122

3'- CGTAGGCACATTA **TAATGTGCCTACG** -5'

Equivalent Sequences - Two sequences such that the second sequence is in the reverse complement of the first sequence

First sequence

SEQ ID No. 123

5'- GCATCCGTGTAAT -3' (A)

Second sequence

SEQ ID No. 124

5'- ATTACACGGATGC -3' (A')

If the first sequence is called A then the second sequence is called A'

Please replace the entire "Examples" section which begins on at the top of page 21 and ends at the end of page 46 with the following amended section (26 pages):

Figures 1 to 14 provide a large number of ways of describing and designing connectron pairs in a genome. We give examples of the description of symmetric and asymmetric connectron pairs in six classes of genomes (prokaryotic, Archeal, single-celled eukaryotic, multi-celled eukaryotic, mammalian and plant). We also give two examples of the design of an asymmetric connectron pair in a single-celled eukaryote and a mammal. It is clear that many other variations of symmetric and asymmetric connectron pairs could be described or designed by someone skilled in the art.

Description of a symmetric lower-upper connectron pair in *E. coli*

E. coli is a prokaryotic organism. A single connectron has been selected from the *E. coli* connectrome to illustrate the properties of a lower-upper connectron pair. Because the connectron is very long it can be split into two connectrons that then bind as a pair. In this and each of the following examples, a header indicates the function of each data field. Because of print-page limitations, the "sequence of match" field has been moved to the left side of each example.

The connectron 1434 has a C1-T1 binding length of 182 bases and a C2-T2 binding length of 171 bases. The shorter of the two matches of 171 bases is then halved with the first half becoming the A and the second half becoming the B in figure 3a producing a producted connectron pair lifetime of 7225.

genome
Connectron id
chromosome
contig
(.groups) id
type
CP = control element on positive strand
CN = control element on negative strand
TP = target element on positive strand
TN = target element on negative strand
match start
match stop
type of Connectron
l/u = lower/upper
l/r = left/right
source of Connectron
g = gene
p = pseudogene
length of match
sequence of match
eco 1434 1 1 7435 CP 4505.026 4505.207 l/u g 182

25 SEQ ID No. 125 CTGTAGATTCAATCTGTCAATGCAACACCCCTTCAATTATCTCTTTCGG
TGTTTTGAACTTCAGTGTCTTTCTCGGTCTGTTGTTAGCTGAGCAGCAA
CCAGATCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGA
AAGTACTGCCGAATTAGCCCATTTGTGTTCTC
eco 1434 1 1 508 TN 279.155 279.336 l/u g 182

30 SEQ ID No. 126 CTGTAGATTCAATCTGTCAATGCAACACCCCTTCAATTATCTCTTTCGG
TGTTTTGAACTTCAGTGTCTTTCTCGGTCTGTTGTTAGCTGAGCAGCAA
CCAGATCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGA
AAGTACTGCCGAATTAGCCCATTTGTGTTCTC
eco 1434 1 1 7435 CP 4505.031 4505.201 l/u g 171

35 SEQ ID No. 127 GATTCAATCTGTCAATGCAACACCCCTTCAATTATCTCTTTCGGTGTTT
TGAACCTTCAGTGTCTTTCTCGGTCTGTTGTTAGCTGAGCAGCAACCAGA
TCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGAAAGTA
CTGCCGAATTAGCCCATTTGT
40 eco 1434 1 1 472 TN 270.811 270.981 l/u g 171

45 SEQ ID No. 128 GATTCAATCTGTCAATGCAACACCCCTTCAATTATCTCTTTCGGTGTTT
TGAACCTTCAGTGTCTTTCTCGGTCTGTTGTTAGCTGAGCAGCAACCAGA
TCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGAAAGTA
CTGCCGAATTAGCCCATTTGT

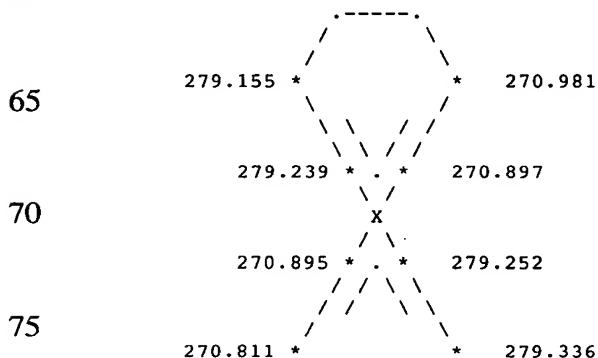
Can form an AB symmetric pair of l/u Connectrons with a lifetime = 85 X 85 = 7225
171

50 SEQ ID No. 129 GATTCAATCTGTCAATGCAACACCCCTTCAATTATCTCTTTCGGTGTTT
TGAACCTTCAGTGTCTTTCTCGGTCTGTTGTTAGCTGAGCAGCAACCAGA
TCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGAAAGTA
CTGCCGAATTAGCCCATTTGT

171

55 SEQ ID No. 130 GATTCAATCTGTCAATGCAACACCCCTTCAATTATCTCTTTCGGTGTTT
TGAACCTTCAGTGTCTTTCTCGGTCTGTTGTTAGCTGAGCAGCAACCAGA
TCTAGTTCATGTTGAGTATATTGGGCAAGACATGTCTTTTAGGAAAGTA
CTGCCGAATTAGCCCATTTGT

279.155 279.239 279.252 279.336 --- 270.811 270.895 270.897 270.981



**Description of a symmetric lower-upper connectron pair
in *S. tokodaii***

S. tokodaii is a Archeal organism. In this and the following
5 examples, the header does not show all the cases for a given
data field.

The connectron 4240 has a C1-T1 binding length of 67 bases and a
C2-T2 binding length of 85 bases. The effective match of 52
10 bases is then halved with the first half becoming the A and the
second half becoming the B in figure 3a producing a producted
connectron pair lifetime of 676.

15 genome
Connectron id
chromosome
contig
(.groups) id
type
match start
match stop
type of Connectron
source of Connectron
length of match
20
25
sto 4240 1 1 3986 CN 1178.996 1179.062 1/u g 67

30 SEQ ID No. 131 TGTACCCCTTCAAGTAAGCCTCATTTAAGGGAGTTTTCTCCCTTGAATA
AACTACCGGGTACATGA

sto 4240 1 1 447 TP 61.903 61.969 1/u g 67

35 SEQ ID No. 132 TGTACCCCTTCAAGTAAGCCTCATTTAAGGGAGTTTTCTCCCTTGAATA
AACTACCGGGTACATGA

40 sto 4240 1 1 3986 CN 1178.963 1179.047 1/u g 85

SEQ ID No. 133 TTGTAATATTATATCAGTTTACTTCTAATATACTGTACCCCTTCAAGTA
AGCCTCATTTAAGGGAGTTTTCTCCCTTGAATAAA

45 sto 4240 1 1 646 TP 123.599 123.683 1/u g 85

SEQ ID No. 134 TTGTAATATTATATCAGTTTACTTCTAATATACTGTACCCCTTCAAGTA
AGCCTCATTTAAGGGAGTTTTCTCCCTTGAATAAA

50

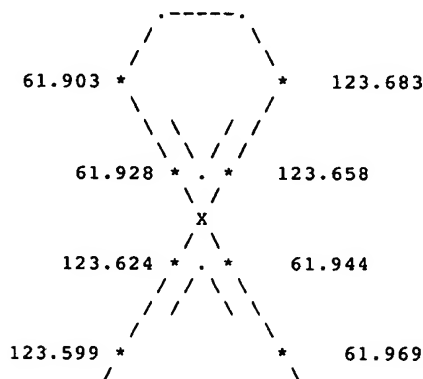
Can form an AB symmetric pair of 1/u Connectrons with a lifetime = 26 X 26 = 676

52

5 SEQ ID No. 135 TGTACCCCTTCAAGTAAGCCTCATTTAAGGGAGTTTCTCCCTTGAATA
AA

10 SEQ ID No. 136 TGTACCCCTTCAAGTAAGCCTCATTTAAGGGAGTTTCTCCCTTGAATA
AA

123.683 61.903 61.928 61.944 61.969 --- 123.599 123.624 123.658



**Description of a symmetric lower-upper connectron pair
in *S. cerevisiae***

The connectron 385 has a C1-T1 binding length of 117 and a C2-T2
35 binding length also of 117 bases. Since the two matches are
equal, the 117 bases are then halved with the first half
becoming the A and the second half becoming the B in figure 3a
producing a producted connectron pair lifetime of 3364.

40 *S. cerevisiae* is a single-celled eukaryotic organism.

45 genome
Connectron id
chromosome
contig
(.groups) id
type
match start
match stop
type of Connectron
source of Connectron
length of match

50

55 yst 385 15 15 28455 CP 975.950 976.066 1/u g 117

sequence of match

60 SEQ ID No. 137 TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG
AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA
ATAGGATCAATGAATAT

yst 385 1 1 419 .TN 165.888 166.004 1/u g 117

65 SEQ ID No. 138 TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG
AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA
ATAGGATCAATGAATAT

yst 385 15 15 28455 CP 975.950 976.066 1/u g 117

70 SEQ ID No. 139 TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG

AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA
 ATAGGATCAATGAATAT

yst 385 1 1 355 TN 160.257 160.373 1/u g 117

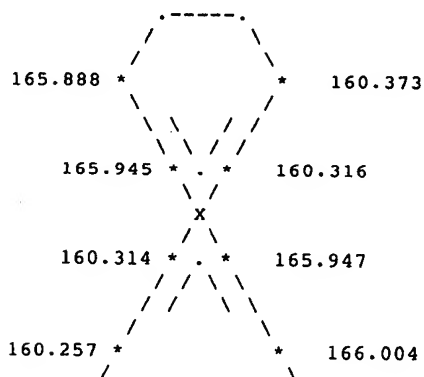
SEQ ID No. 140 TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG
 AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA
 ATAGGATCAATGAATAT

Can form an AB symmetric pair of 1/u Connectrons with a lifetime = $58 \times 58 = 3364$

SEQ ID No. 141 TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG
 AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA
 ATAGGATCAATGAATAT

SEQ ID No. 142 TTACTAGTATATTATCATATACGGTGTTAGAAGATGACGCAAATGATGAG
 AAATAGTCATCTAAATTAGTGGAAGCTGAAACGCAAGGATTGATAATGTA
 ATAGGATCAATGAATAT

165.888 165.945 165.947 166.004 --- 160.257 160.314 160.316 160.373



50 Description of a symmetric lower-upper connectron pair in *C. elegans*

C. elegans is a 1,000-celled eukaryotic organism.

55 The connectron 55 has a C1-T1 binding length of 68 and a C2-T2 binding length also of 68 bases. The effective match of 43 bases is then halved with the first half becoming the A and the second half becoming the B in figure 3a producing a producted connectron pair lifetime of 441.

genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match										
wrm	55	1	1	380 CN	221.205	221.272	1/u g			68

SEQ ID No. 143 GGGAATTGCTTCGTCAAATGATCGACGGAGGGCTTTGGCCATCTGCAAG
GATAAACTCGCATGTCGA

wrm 55 1 1 433 TN 250.979 251.046 1/u g 68

SEQ ID No. 144 GGGAATTGCTTCGTCAAATGATCGACGGAGGGCTTTGGCCATCTGCAAG
GATAAACTCGCATGTCGA

wrm 55 1 1 380 CN 221.180 221.247 1/u g 68

SEQ ID No. 145 GAGCTCGCAACACCGGCCGAGCAGCGGAATTGCTTCGTCAAATGATCGA
CGGAGGGCTTTGGCCAT

wrm 55 1 1 354 TN 214.904 214.971 1/u g 68

SEQ ID No. 146 GAGCTCGCAACACCGGCCGAGCAGCGGAATTGCTTCGTCAAATGATCGA
CGGAGGGCTTTGGCCAT

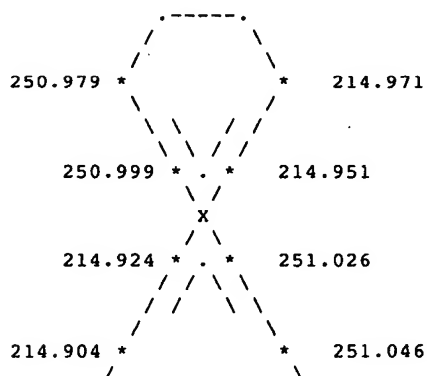
Can form an AB symmetric pair of 1/u Connectrons with a lifetime = 21 X 21 = 441
43

SEQ ID No. 147 GGGAATTGCTTCGTCAAATGATCGACGGAGGGCTTTGGCCAT

43

SEQ ID No. 148 GGGAATTGCTTCGTCAAATGATCGACGGAGGGCTTTGGCCAT

250.979 250.999 251.026 251.046 --- 214.904 214.924 214.951 214.971



Description of a symmetric lower-upper connectron pair in *H. sapiens*

H. sapiens is a multi-celled eukaryotic organism - a mammal.

The connectron 1211 has a C1-T1 binding length of 58 bases and a C2-T2 binding length also of 58 bases. Since the two matches are equal, 58 is then halved with the first half becoming the A and the second half becoming the B in figure 3a producing a producted connectron pair lifetime of 841.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
hsd	1211	4	1	1331 CP	16.381	16.438	l/u	g	58

SEQ ID No. 149 GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT
AAAGATCA

hsd	1211	4	1	1542 TP	500.217	500.274	l/u	g	58
-----	------	---	---	---------	---------	---------	-----	---	----

SEQ ID No. 150 GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT
AAAGATCA

hsd	1211	4	1	1331 CP	16.381	16.438	l/u	g	58
-----	------	---	---	---------	--------	--------	-----	---	----

SEQ ID No. 151 GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT
AAAGATCA

hsd	1211	4	1	1559 TP	504.937	504.994	l/u	g	58
-----	------	---	---	---------	---------	---------	-----	---	----

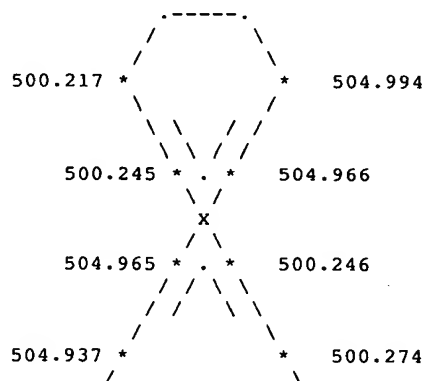
SEQ ID No. 152 GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT
AAAGATCA

Can form an AB symmetric pair of l/u Connectrons with a lifetime = $29 \times 29 = 841$

SEQ ID No. 153 GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT
AAAGATCA

SEQ ID No. 154 GGTGAGTACCTTTCTATGAAGGTGATAAGGATCCACTGAGTCTTCCATAT
AAAGATCA

500.217 500.245 500.246 500.274 --- 504.937 504.965 504.966 504.994



Description of a symmetric lower-upper connectron pair
in *A. thaliana*

A. thaliana is a multi-celled eukaryotic organism - a plant.

The connectron 3 has a C1-T1 binding length of 94 bases and a
C2-T2 binding length of 79 bases. The shorter of the two
matches of 79 bases is then halved with the first half becoming

the A and the second half becoming the B in figure 5a producing a producted connectron pair lifetime of 1521.

```

5 genome
  |
  |
10 Connectron id
   |
   | chromosome
   |
   | contig
   |
   | (.groups) id
   | type
   |
   | match start
   |
   | match stop
   | type of Connectron
   | source of Connectron
   | length of match
15 sequence of match
   |
   | ath
   |
   | 3
   |
   | 5
   |
   | 1
   |
   | 29822 CN
   |
   | 21590.870
   |
   | 21590.960
   |
   | 1/u q
   |
   | 94

```

SEQ ID No. 155 TGTGAAAGTTAAACTTGATTTTGAATCAAGTTAATTATTGGATCAATT
ATCCAATAATTAATTAGGCCAAATCCAAGTTCTAGAGTTTTC

ath	3	1	1	7951 TP	3780.765	3780.858	1/u q	94
-----	---	---	---	---------	----------	----------	-------	----

SEQ ID No. 156 TGTGTAAAGTTAAACTTGATTTTGAATCAAGTTAATTATTGGATCAATT
ATCCAATAATTAATTATGGCCAAATCCAAGTTCTAGAGTTTCT

ath	3	5	1	29822 CN	21590.870	21590.950	1/u g	79
-----	---	---	---	----------	-----------	-----------	-------	----

SEQ ID No. 157 TGTGTAAAGTTAACTTGATTTTGAATCAAGTTAATTATTGGATCAATT
ATCCAATAATTAATTATGGCCAAATCCAA

ath	3	1	1	7985 TP	3785.281	3785.359	1/u g	79
-----	---	---	---	---------	----------	----------	-------	----

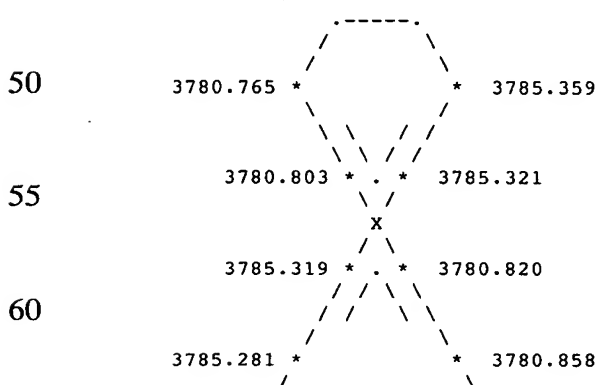
SEQ ID No. 158 TGTGTGAAGTTAAACTTGATTTTGAATCAAGTTTAATTATTGGATCAATT
ATCCAATAATTAATTATGGCCAAATCCAA

Can form an AB symmetric pair of 1/u Connectrons with a lifetime = $39 \times 39 = 1521$

SEQ ID No. 159 TGTGAAAGTTAACTTGATTTGAATCAAGTTTAATTATTGGATCAATT
ATCCAATAATTAATTATGGCCAAATCCAA

SEQ ID No. 160 TGGTTGAAAGTTAACTTGATTTTGAATCAAGTTAATTATTGGATCAATT
ATCCAATAATTAATTATGGCCAAATCCAA

45	3785.359	3780.765	3780.803	3780.820	3780.858 ---	3785.281	3785.319	3785.321
----	----------	----------	----------	----------	--------------	----------	----------	----------



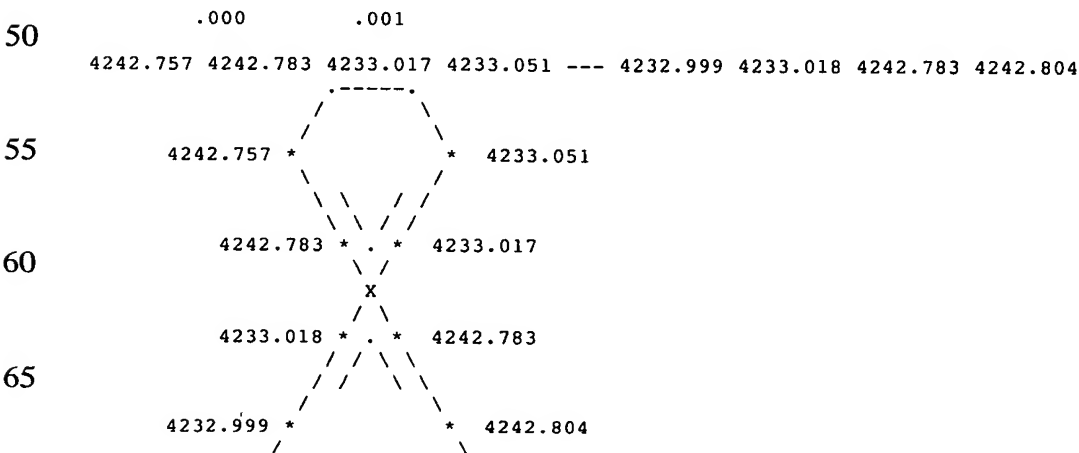
65 Description of an asymmetric lower-upper connectron pair in *E. coli*

The connectron 14918 has a C1-T1 binding length of 27 bases and a C2-T2 binding length of 35 bases. The shorter of the two matches at 27 bases produces the lifetime for this connectron. The connectron 15118 has a C1-T1 binding length of 20 bases and

a C2-T2 binding length of 22 bases. The shorter of the two matches at 20 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 9d is 540.

5	genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
	sequence of match				type					
	eco 14918	1	1	7316 CN	4454.807	4454.833	1/u g		27	
20	<u>SEQ ID No. 161</u>									
	eco 14918	1	1	6955 TN	4242.757	4242.783	1/u g		27	
	<u>SEQ ID No. 162</u>									
25	eco 14918	1	1	7316 CN	4454.810	4454.844	1/u g		35	
	<u>SEQ ID No. 163</u>									
	eco 14918	1	1	6937 TN	4233.017	4233.051	1/u g		35	
	<u>SEQ ID No. 164</u>									
30	eco 15118	1	1	1544 CP	831.575	831.594	1/u g		20	
	<u>SEQ ID No. 165</u>									
35	eco 15118	1	1	6939 TP	4232.999	4233.018	1/u g		20	
	<u>SEQ ID No. 166</u>									
40	eco 15118	1	1	1544 CP	831.596	831.617	1/u g		22	
	<u>SEQ ID No. 167</u>									
	eco 15118	1	1	6957 TP	4242.783	4242.804	1/u g		22	
45	<u>SEQ ID No. 168</u>									

Found L/U AD AB - CD Connectron pair for 14918 and 15118 with a lifetime = 27 X 20 = 540



Description of an asymmetric lower-upper connectron pair in *S. tokodaii*

The connectron 6416 has a C1-T1 binding length of 59 bases and a C2-T2 binding length of 60 bases. The shorter of the two matches at 59 bases produces the lifetime for this connectron. The connectron 6477 has a C1-T1 binding length of 189 bases and a C2-T2 binding length of 36 bases. The shorter of the two matches at 36 bases produces the lifetime for this connectron. The lifetime of this pair of dominant - anti-dominant connectrons as shown in figure 9d is 2124.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sto	6416	1	1	3245 CP	1036.523	1036.581	1/u g		59

SEQ ID No. 169 ACTCCCAGTGAGGGATAGGGGTAACGGACTGAAGACCCAGCCCGTGGTCT

ACCGCTGGA

sto	6416	1	1	3439 TP	1079.594	1079.652	1/u g	59
-----	------	---	---	---------	----------	----------	-------	----

SEQ ID No. 170 ACTCCCAGTGAGGGATAGGGGTAACGGACTGAAGACCCAGCCCGTGGTCT

ACCGCTGGA

sto	6416	1	1	3250 CP	1036.635	1036.694	1/u g	60
-----	------	---	---	---------	----------	----------	-------	----

SEQ ID No. 171 ATGAAGGTGGTAAACCACAAACCTATGAACCGCCCTAAGGGAACCCCTCGC

CCTTTAGGGC

sto	6416	1	1	3714 TP	1146.360	1146.419	1/u g	60
-----	------	---	---	---------	----------	----------	-------	----

SEQ ID No. 172 ATGAAGGTGGTAAACCACAAACCTATGAACCGCCCTAAGGGAACCCCTCGC

CCTTTAGGGC

sto	6477	1	1	618 CN	120.361	120.549	1/u g	189
-----	------	---	---	--------	---------	---------	-------	-----

SEQ ID No. 173 CTATCCCTCACCAAGAGTTGCCCTCTGCTCTTGGCTCTTGGGGACTCGGG

GATATGTAGTTCTGTGCGGGACACATATCTTCAGTATGCCCACCTTTGT

GGGCTTCCCCGCACTTTATTAATAGTTTAAAGCTAAGATTAAAACTTTA

CCCCGCCTTAAAGGCGAGGCTTGCCCCGCGTTTGTCA

sto	6477	1	1	3709 TN	1146.169	1146.357	1/u g	189
-----	------	---	---	---------	----------	----------	-------	-----

SEQ ID No. 174 CTATCCCTCACCAAGAGTTGCCCTCTGCTCTTGGCTCTTGGGGACTCGGG

GATATGTAGTTCTGTGCGGGACACATATCTTCAGTATGCCCACCTTTGT

GGGCTTCCCCGCACTTTATTAATAGTTTAAAGCTAAGATTAAAACTTTA

CCCCGCCTTAAAGGCGAGGCTTGCCCCGCGTTTGTCA

sto	6477	1	1	622 CN	120.590	120.625	1/u g	36
-----	------	---	---	--------	---------	---------	-------	----

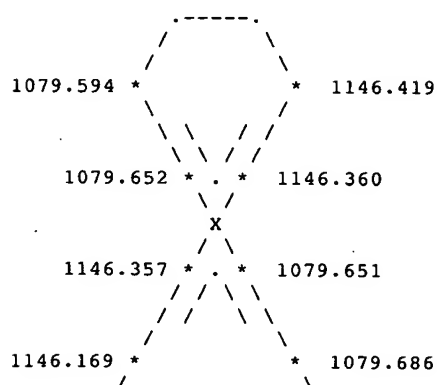
SEQ ID No. 175 CACCCACCCGCTCCGTTTCGTCCAGCGGTAGACCAC

sto	6477	1	1	3446 TN	1079.651	1079.686	1/u g	36
-----	------	---	---	---------	----------	----------	-------	----

SEQ ID No. 176 CACCCACCCGCTCCGTTTCGTCCAGCGGTAGACCAC

.001 .003

1079.594 1079.652 1146.360 1146.419 --- 1146.169 1146.357 1079.651 1079.686



**Description of an asymmetric lower-upper connectron pair
in *S. cerevisiae***

The connectron 3814 has a C1-T1 binding length of 72 bases and a C2-T2 binding length of 72 bases. The either of the two matches at 72 bases produces the lifetime for this connectron. The connectron 3847 has a C1-T1 binding length of 81 bases and a C2-T2 binding length of 89 bases. The shorter of the two matches at 81 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 9d is 5832.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match				type					
yst	3814	13	13	23498 CP	362.701	362.772	1/u g		72

SEQ ID No. 177 ATGGAATCTATATTTCTACATACTAATATTACGATTATTCCTCATTCGGT
TTTATATGTTTCATTATCCTAT

yst	3814	2	2	1896 TN	265.267	265.338	1/u g		72
-----	------	---	---	---------	---------	---------	-------	--	----

SEQ ID No. 178 ATGGAATCTATATTTCTACATACTAATATTACGATTATTCCTCATTCGGT
TTTATATGTTTCATTATCCTAT

yst	3814	13	13	23498 CP	362.701	362.772	1/u g		72
-----	------	----	----	----------	---------	---------	-------	--	----

SEQ ID No. 179 ATGGAATCTATATTTCTACATACTAATATTACGATTATTCCTCATTCGGT
TTTATATGTTTCATTATCCTAT

yst	3814	2	2	1495 TN	226.820	226.891	1/u g		72
-----	------	---	---	---------	---------	---------	-------	--	----

SEQ ID No. 180 ATGGAATCTATATTTCTACATACTAATATTACGATTATTCCTCATTCGGT
TTTATATGTTTCATTATCCTAT

yst	3847	13	13	23551 CN	372.772	372.852	1/u g	81
-----	------	----	----	----------	---------	---------	-------	----

5 SEQ ID No. 181 AAACATATAAAACGGAATGAGGAATAATCGTAATATTAGTATGTAGAAAT
ATAGATTCCATTTTGAGGATTCCTATATCCT

yst	3847	2	2	1496 TP	226.739	226.819	1/u g	81
-----	------	---	---	---------	---------	---------	-------	----

10 SEQ ID No. 182 AAACATATAAAACGGAATGAGGAATAATCGTAATATTAGTATGTAGAAAT
ATAGATTCCATTTTGAGGATTCCTATATCCT

yst	3847	13	13	23551 CN	372.836	372.924	1/u g	89
-----	------	----	----	----------	---------	---------	-------	----

15 SEQ ID No. 183 GAGGATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTATACCTA
ATATTATAGCCTTTATCAACAATGGAATCCCAACAATTA

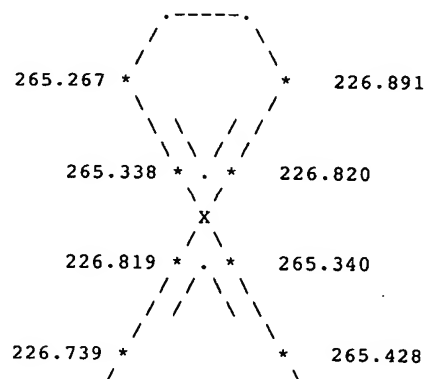
yst	3847	2	2	1923 TP	265.340	265.428	1/u g	89
-----	------	---	---	---------	---------	---------	-------	----

20 SEQ ID No. 184 GAGGATTCCTATATCCTCGAGGAGAACTTCTAGTATATTCTGTATACCTA
ATATTATAGCCTTTATCAACAATGGAATCCCAACAATTA

25 Found L/U AD AB - CD Connectron pair for 3814 and 3847 with a lifetime = 72 X 81 = 5832

.002 .001

30 265.267 265.338 226.820 226.891 --- 226.739 226.819 265.340 265.428



50 **Description of an asymmetric lower-upper connectron pair
in *C. elegans***

The connectron 23175 has a C1-T1 binding length of 15 bases and
55 a C2-T2 binding length of 18 bases. The shorter of the two
matches at 15 bases produces the lifetime for this connectron.

The connectron 23179 has a C1-T1 binding length of 16 bases and
a C2-T2 binding length of 19 bases. The shorter of the two
matches at 16 bases produces the lifetime for this connectron.

60 The lifetime of this pair of dominant - anti-dominant
connectrons as shown in figure 9c is 240.

genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match										
wrm	23175	4	2	22854	CP	708.778	708.792	1/u	g	15

SEQ ID No. 185

TGGTCTGCTAAATCG

wrm 23175 4

2 21925 TP 415.203 415.217 1/u g 15

20 SEQ ID No. 186

TGGTCTGCTAAATCG

wrm 23175 4

2 22854 CP 708.793 708.810 1/u g 18

25 SEQ ID No. 187

AAACTTGTAGTTTGTAGT

wrm 23175 4

2 22166 TP 486.479 486.496 1/u g 18

SEQ ID No. 188

AAACTTGTAGTTTGTAGT

30

wrm 23179 4

2 24763 CN 1373.569 1373.584 1/u g 16

35 SEQ ID No. 189

ATTTAGCAGACCCAAA

wrm 23179 4

2 22165 TN 486.461 486.476 1/u g 16

SEQ ID No. 190

ATTTAGCAGACCCAAA

40 wrm 23179 4

2 24763 CN 1373.554 1373.572 1/u g 19

SEQ ID No. 191

AAACTACAAATTTTCGATTT

45 wrm 23179 4

2 21926 TN 415.212 415.230 1/u g 19

SEQ ID No. 192

AAACTACAAATTTTCGATTT

50

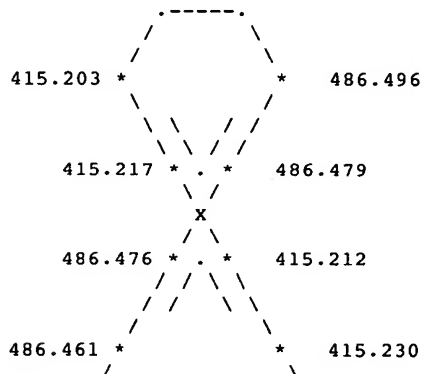
Found L/U DA AB - CD Connectron pair for 23175 and 23179 with a lifetime = 15 X 16 = 240

.005 .003

55

415.203 415.217 486.479 486.496 --- 486.461 486.476 415.212 415.230

60



65

70

**Description of an asymmetric lower-upper connectron pair
in *H. sapiens***

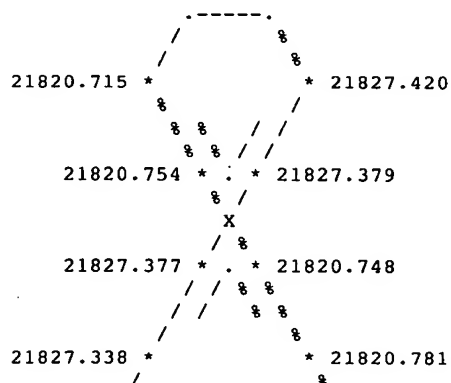
5 The connectron 383992 has a C1-T1 binding length of 39 bases and
a C2-T2 binding length of 41 bases. The shorter of the two
matches at 39 bases produces the lifetime for this connectron.
The connectron 383993 has a C1-T1 binding length of 40 bases and
a C2-T2 binding length of 34 bases. The shorter of the two
10 matches at 34 bases produces the lifetime for this connectron.
The lifetime of this pair of dominant - anti-dominant
connectrons as shown in figure 9c is 1326.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match				type					
hsd 383992 920	19 756303 CP 21789.055 21789.092	u/d g	39						
<hr/>									
SEQ ID No. 193	AGCCCCGAGCCCCACCTCTCCCTTAGGGACCTCCGCCAC								
hsd 383992 920	19 756563 TP 21820.715 21820.754	u/d g	39						
SEQ ID No. 194	AGCCCCGAGCCCCACCTCTCCCTTAGGGACCTCCGCCAC								
hsd 383992 920	19 756303 CP 21789.080 21789.121	u/d g	41						
SEQ ID No. 195	ACCTCCGCCCCACCTACCTCAAGCCAGGATGCCCGGAGCG								
hsd 383992 920	19 756615 TP 21827.379 21827.420	u/d g	41						
SEQ ID No. 196	ACCTCCGCCCCACCTACCTCAAGCCAGGATGCCCGGAGCG								
<hr/>									
hsd 383993 920	19 756433 CN 21808.781 21808.820	u/d g	40						
SEQ ID No. 197	CCTAAGGGAGAGGTGGGGCTCGGGCTGAATCCCTCGTTGG								
hsd 383993 920	19 756614 TN 21827.338 21827.377	u/d g	40						
SEQ ID No. 198	CCTAAGGGAGAGGTGGGGCTCGGGCTGAATCCCTCGTTGG								
hsd 383993 920	19 756433 CN 21808.740 21808.773	u/d g	34						
SEQ ID No. 199	GCTCCGGGCATCCTGGCTTGAGGGTAGAGTGGGC								
hsd 383993 920	19 756564 TN 21820.748 21820.781	u/d g	34						
SEQ ID No. 200	GCTCCGGGCATCCTGGCTTGAGGGTAGAGTGGGC								

Found L/U DA AB - CD Connectron pair for 383992 and 383993 with a lifetime = 39 X 34 = 1326

0.006 0.002

21820.715 21820.754 21827.379 21827.420 --- 21827.338 21827.377 21820.748 21820.781



Description of an asymmetric lower-upper connectron pair in *A. thaliana*

The connectron 188312 has a C1-T1 binding length of 20 bases and a C2-T2 binding length of 30 bases. The shorter of the two matches at 20 bases produces the lifetime for this connectron.

The connectron 188397 has a C1-T1 binding length of 30 bases and a C2-T2 binding length of 16 bases. The shorter of the two matches at 16 bases produces the lifetime for this connectron.

The lifetime of this pair of dominant - anti-dominant connectrons as shown in figure 9c is 340.

genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
ath	188312	18	4	269631	CP	5320.517	5320.536	u/d	g	20

SEQ ID No. 201

TTGTAGACGTATGGTGGTGG

ath	188312	18	4	269507	TP	5311.160	5311.179	u/d	g	20
-----	--------	----	---	--------	----	----------	----------	-----	---	----

SEQ ID No. 202

TTGTAGACGTATGGTGGTGG

ath	188312	18	4	269631	CP	5320.519	5320.548	u/d	g	30
-----	--------	----	---	--------	----	----------	----------	-----	---	----

SEQ ID No. 203

GTAGACGTATGGTGGTGGGAGACTTGA

ath	188312	18	4	269890	TP	5340.361	5340.390	u/d	g	30
-----	--------	----	---	--------	----	----------	----------	-----	---	----

SEQ ID No. 204

GTAGACGTATGGTGGTGGGAGACTTGA

ath	188397	18	4	269741	CN	5324.883	5324.921	u/d	g	39
-----	--------	----	---	--------	----	----------	----------	-----	---	----

SEQ ID No. 205

GCTCTCCACCACCACCATACTACAGTCCATCTCCAAAGG

ath 188397 18 4 269881 TN 5340.322 5340.360 u/d g 39

SEQ ID No. 206

GCTCTCCACCACCACCATACTACAGTCCATCTCCAAAGG

ath 188397 18 4 269741 CN 5324.867 5324.882 u/d g 16

SEQ ID No. 207

CCACCATACGTCTACA

ath 188397 18 4 269509 TN 5311.176 5311.191 u/d g 16

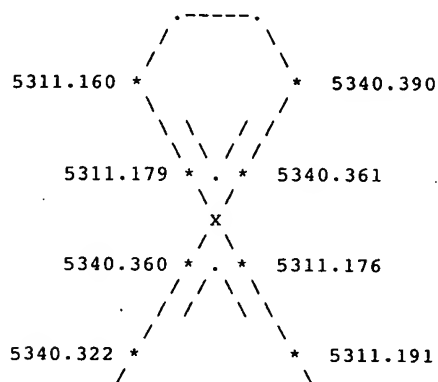
SEQ ID No. 208

CCACCATACGTCTACA

Found L/U DA AB - CD Connectron pair for 188312 and 188397 with a lifetime = 20 X 16 = 320

0.003 0.001

5311.160 5311.179 5340.361 5340.390 --- 5340.322 5340.360 5311.176 5311.191

**Description of an asymmetric left-right connectron pair in E. coli**

The connectron 3707 has a C1-T1 binding length of 21 bases and a C2-T2 binding length of 19 bases. The shorter of the two matches at 19 bases produces the lifetime for this connectron.

The connectron 3763 has a C1-T1 binding length of 42 bases and a C2-T2 binding length of 37 bases. The shorter of the two matches at 37 bases produces the lifetime for this connectron.

The lifetime of this pair of dominant - dominant connectrons as shown in figure 10a is 703.

genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connection	source of Connection	length of match
eco	3707	1	1	3906	CN	2338.350	2338.370	l/r g	21	

SEQ ID No. 209

AACGCCTTATCCGGCCTACGG

eco	3707	1	1	689	TP	374.169	374.189	l/r g	21	
-----	------	---	---	-----	----	---------	---------	-------	----	--

SEQ ID No. 210

AACGCCTTATCCGGCCTACGG

eco	3707	1	1	3906	CN	2338.380	2338.398	l/r g	19	
-----	------	---	---	------	----	----------	----------	-------	----	--

SEQ ID No. 211

GTAGGCCTGATAAGACGCG

eco	3707	1	1	707	TN	376.619	376.637	l/r g	19	
-----	------	---	---	-----	----	---------	---------	-------	----	--

SEQ ID No. 212

GTAGGCCTGATAAGACGCG

eco	3763	1	1	709	CP	376.712	376.753	l/r g	42	
-----	------	---	---	-----	----	---------	---------	-------	----	--

SEQ ID No. 213

GTAGGCCGGATAAGGCGTTCACGCCGCATCCGGCAGTCGTGC

eco	3763	1	1	690	TN	374.152	374.193	l/r g	42	
-----	------	---	---	-----	----	---------	---------	-------	----	--

SEQ ID No. 214

GTAGGCCGGATAAGGCGTTCACGCCGCATCCGGCAGTCGTGC

eco	3763	1	1	709	CP	376.717	376.753	l/r g	37	
-----	------	---	---	-----	----	---------	---------	-------	----	--

SEQ ID No. 215

CCGGATAAGGCGTTCACGCCGCATCCGGCAGTCGTGC

eco	3763	1	1	706	TP	376.617	376.653	l/r g	37	
-----	------	---	---	-----	----	---------	---------	-------	----	--

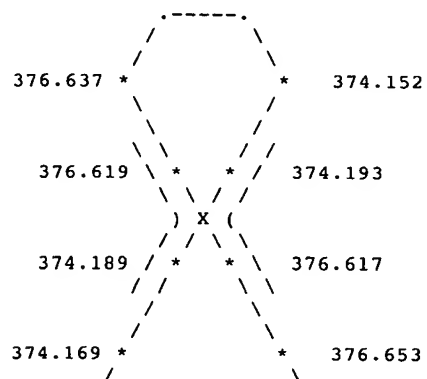
SEQ ID No. 216

CCGGATAAGGCGTTCACGCCGCATCCGGCAGTCGTGC

Found L/R DD AB - CD Connectron pair for 3707 and 3763 with a lifetime = 19 x 37 = 703

.004 .002

374.169 374.189 376.619 376.637 --- 374.152 374.193 376.617 376.653



Description of an asymmetric left-right connectron pair in *S. cerevisiae*

The connectron 6834 has a C1-T1 binding length of 105 bases and a C2-T2 binding length of 38 bases. The shorter of the two matches at 38 bases produces the lifetime for this connectron. The connectron 6944 has a C1-T1 binding length of 152 bases and a C2-T2 binding length of 143 bases. The shorter of the two matches at 143 bases produces the lifetime for this connectron. The lifetime of this pair of dominant - anti-dominant connectrons as shown in figure 10c is 5434.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match									
yst 6834	7	7	10928 CN	111.321	111.425	1/r g		105	

SEQ ID No. 217 CGGTGTTAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTG
GAAGCTGAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAAC
ATATA
yst 6834 3 3 2988 TP 84.359 84.463 1/r g 105

SEQ ID No. 218 CGGTGTTAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTG
GAAGCTGAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAAC
ATATA
yst 6834 7 7 10945 CN 111.449 111.486 1/r g 38

SEQ ID No. 219 TCATCTACTAACTAGTATTTACGTTACTAGTATATTAT
yst 6834 3 3 3500 TN 168.765 168.802 1/r g 38

SEQ ID No. 220 TCATCTACTAACTAGTATTTACGTTACTAGTATATTAT

yst 6944 4 4 5116 CN 645.641 645.792 1/r g 152

SEQ ID No. 221 TCATCTACTAACTAGTATTTACGTTACTAGTATATTATCATATACGGTGT
TAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCT
GAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAACATATAA
AA
yst 6944 3 3 2991 TP 84.315 84.466 1/r g 152

SEQ ID No. 222 TCATCTACTAACTAGTATTTACGTTACTAGTATATTATCATATACGGTGT
TAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCT
GAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAACATATAA
AA
yst 6944 4 4 5116 CN 645.641 645.783 1/r g 143

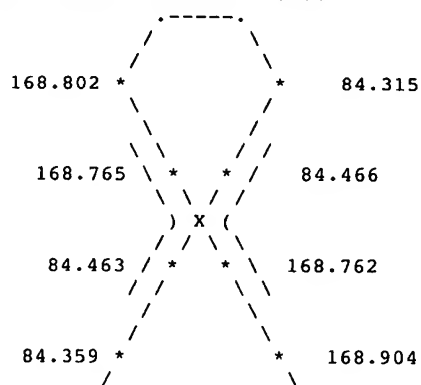
SEQ ID No. 223 TCATCTACTAACTAGTATTTACGTTACTAGTATATTATCATATACGGTGT
TAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCT
GAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAACATATAA
AA
yst 6944 3 3 3496 TN 168.762 168.904 1/r g 143

SEQ ID No. 224 TCATCTACTAACTAGTATTTACGTTACTAGTATATTATCATATACGGTGT
TAGAAGATGACGCAAATGATGAGAAATAGTCATCTAAATTAGTGGAAGCT
GAAACGCAAGGATTGATAATGTAATAGGATCAATGAATATTAACATATAA
AA

Found L/R DA AB - CD Connectron pair for 6834 and 6944 with a lifetime = $38 \times 143 = 5434$

.003 .003

84.359 84.463 168.765 168.802 --- 84.315 84.466 168.762 168.904



Description of an asymmetric left-right connectron pair
in *C. elegans*

The connectron 40849 has a C1-T1 binding length of 34 bases and a C2-T2 binding length of 34 bases. The either of the two matches at 34 bases produces the lifetime for this connectron. The connectron 40850 has a C1-T1 binding length of 48 bases and a C2-T2 binding length of 39 bases. The shorter of the two matches at 39 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 10d is 1326.

genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match										
wrm	40849	6	2	51392	CN	13819.470	13819.500	l/r	g	34
<u>SEQ ID No. 225</u>										
ACCGAACCCAACGGCCCTCTTTAGGGCCACAAAT										
wrm	40849	6	2	51379	TN	13817.594	13817.630	l/r	g	34
<u>SEQ ID No. 226</u>										
ACCGAACCCAACGGCCCTCTTTAGGGCCACAAAT										
wrm	40849	6	2	51392	CN	13819.470	13819.500	l/r	g	34
<u>SEQ ID No. 227</u>										
ACCGAACCCAACGGCCCTCTTTAGGGCCACAAAT										
wrm	40849	6	2	51400	TP	13820.550	13820.583	l/r	g	34
<u>SEQ ID No. 228</u>										
ACCGAACCCAACGGCCCTCTTTAGGGCCACAAAT										

wrm 40850 6 2 51410 CN 13820.791 13820.840 l/r g 48

SEQ ID No. 229 CAACACACCTAACCGAACCCAACGGCCCTCTTTAGGGCCACAAATGTT

wrm 40850 6 2 51379 TN 13817.583 13817.630 l/r g 48

SEQ ID No. 230 CAACACACCTAACCGAACCCAACGGCCCTCTTTAGGGCCACAAATGTT

wrm 40850 6 2 51410 CN 13820.800 13820.840 l/r g 39

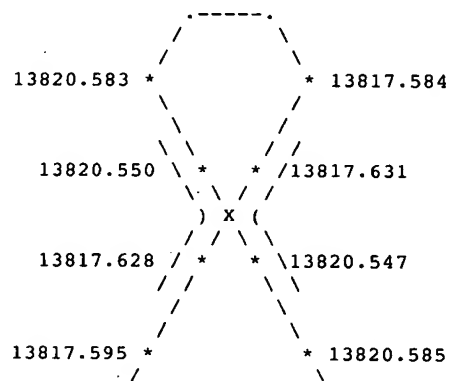
SEQ ID No. 231 CTAACCGAACCCAACGGCCCTCTTTAGGGCCACAAATGT

wrm 40850 6 2 51400 TP 13820.550 13820.584 l/r g 39

SEQ ID No. 232 CTAACCGAACCCAACGGCCCTCTTTAGGGCCACAAATGT

Found L/R AD AB - CD Connectron pair for 40849 and 40850 with a lifetime = 34 X 39 = 1326
.003 .003

13817.595 13817.628 13820.550 13820.583 --- 13817.584 13817.631 13820.547 13820.585



Description of an asymmetric left-right connectron pair in *H. sapiens*

The connectron 67620 has a C1-T1 binding length of 38 bases and a C2-T2 binding length of 33 bases. The shorter of the two matches at 33 bases produces the lifetime for this connectron. The connectron 67621 has a C1-T1 binding length of 41 bases and a C2-T2 binding length of 42 bases. The shorter of the two matches at 41 bases produces the lifetime for this connectron. The lifetime of this pair of dominant - anti-dominant connectrons as shown in figure 10c is 1353.

genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
hsd	67620	100	1	96091	CN	1705.996	1706.033	l/r	g	38

SEQ ID No. 233

GTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGC

hsd	67620	60	1	78101	TP	218.397	218.434	l/r	g	38
-----	-------	----	---	-------	----	---------	---------	-----	---	----

SEQ ID No. 234

GTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGC

hsd	67620	100	1	96101	CN	1705.970	1706.002	l/r	g	33
-----	-------	-----	---	-------	----	----------	----------	-----	---	----

SEQ ID No. 235

AGGTCAGGAGATCGAGACCATCCTGGCTAACAC

hsd	67620	60	1	78110	TN	234.341	234.373	l/r	g	33
-----	-------	----	---	-------	----	---------	---------	-----	---	----

SEQ ID No. 236

AGGTCAGGAGATCGAGACCATCCTGGCTAACAC

hsd	67621	100	1	98781	CN	3142.085	3142.125	l/r	g	41
-----	-------	-----	---	-------	----	----------	----------	-----	---	----

SEQ ID No. 237

CGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCC

hsd	67621	60	1	78101	TP	218.395	218.435	l/r	g	41
-----	-------	----	---	-------	----	---------	---------	-----	---	----

SEQ ID No. 238

CGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCC

hsd	67621	100	1	98781	CN	3142.052	3142.093	l/r	g	42
-----	-------	-----	---	-------	----	----------	----------	-----	---	----

SEQ ID No. 239

GAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAAC

hsd	67621	60	1	78110	TN	234.340	234.381	l/r	g	42
-----	-------	----	---	-------	----	---------	---------	-----	---	----

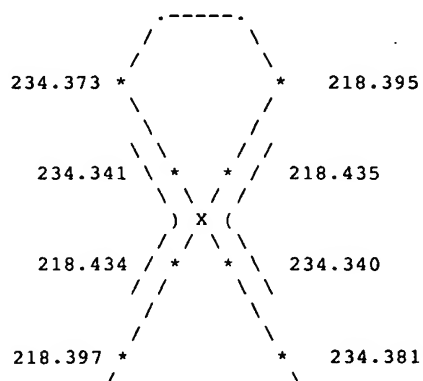
SEQ ID No. 240

GAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAAC

Found L/R DA AB - CD Connectron pair for 67620 and 67621 with a lifetime = 33 X 41 = 1353

0.001 0.001

218.397 218.434 234.341 234.373 --- 218.395 218.435 234.340 234.381



Description of an asymmetric left-right connectron pair
in *A. thaliana*

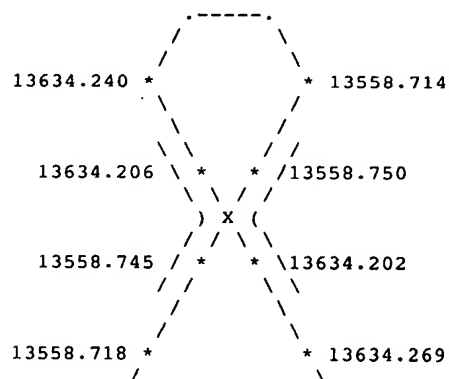
The connectron 5 has a C1-T1 binding length of 28 bases and a C2-T2 binding length of 35 bases. The shorter of the two matches at 28 bases produces the lifetime for this connectron. The connectron 6 has a C1-T1 binding length of 37 bases and a C2-T2 binding length of 68 bases. The shorter of the two matches at 37 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 10d is 1036.

genome	Connectron id	chromosome	contig	(.groups) id	type	match start	match stop	type of Connectron	source of Connectron	length of match
ath	5	15	3	102175	CN	12540.150	12540.174	1/r	g	28
<u>SEQ ID No. 241</u>										
ATCATCAATGAACTCATTGGCTAAGGT										
ath	5	15	3	102902	TN	13558.720	13558.750	1/r	g	28
<u>SEQ ID No. 242</u>										
ATCATCAATGAACTCATTGGCTAAGGT										
ath	5	15	3	102176	CN	12540.184	12540.220	1/r	g	35
<u>SEQ ID No. 243</u>										
ACATTCATTAGTTCTGGAACGTGAATCAAGCAATG										
ath	5	15	3	103090	TP	13634.210	13634.240	1/r	g	35
<u>SEQ ID No. 244</u>										
ACATTCATTAGTTCTGGAACGTGAATCAAGCAATG										

ath	6	15	3	103067	CP	13626.660	13626.700	1/r	g	37
<u>SEQ ID No. 245</u>										
ATGCATCATCAATGAACTCATTGGCTAAGGTGAAGG										
ath	6	15	3	102902	TN	13558.713	13558.750	1/r	g	37
<u>SEQ ID No. 246</u>										
ATGCATCATCAATGAACTCATTGGCTAAGGTGAAGG										
ath	6	15	3	103067	CP	13626.624	13626.691	1/r	g	68
<u>SEQ ID No. 247</u>										
AACTCATTGGCTAAGGT										
ath	6	15	3	103090	TP	13634.202	13634.270	1/r	g	68
<u>SEQ ID No. 248</u>										
TTTAACATTCATTAGTTCTGGAACGTGAATCAAGCAATGCATCATCAATG										
AACTCATTGGCTAAGGT										

Found L/R AD AB - CD Connectron pair for 5 and 6 with a lifetime = $28 \times 37 = 1036$
 .005 .004

5 13558.718 13558.745 13634.206 13634.240 --- 13558.714 13558.750 13634.202 13634.269



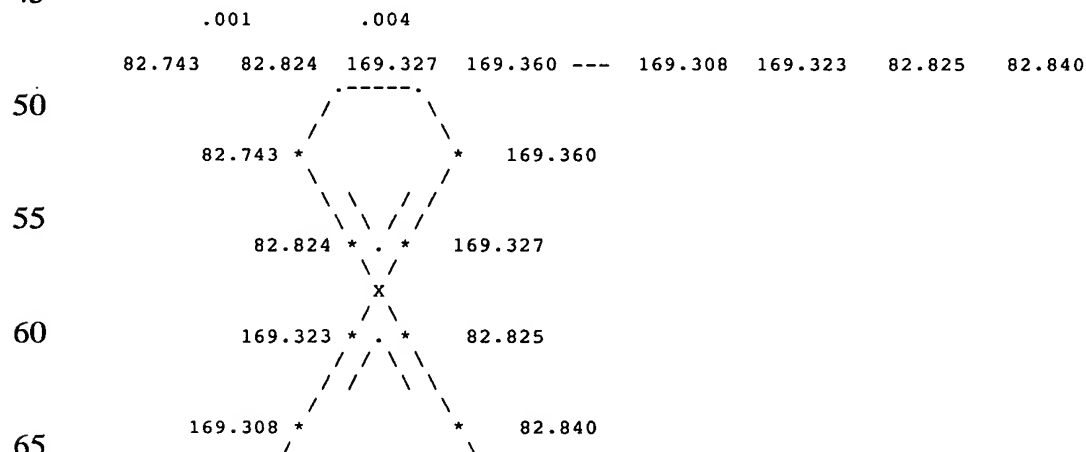
Design of an asymmetric lower-upper connectron pair in *S. cerevisiae*

There are many ways to design a pair of connectrons. In this example we have chosen to replace the C1 source and the T1 target of the upper naturally occurring connectron with another sequence. Design of a connectron pair can be accomplished by anyone skilled the art by modifying and/or replacing any of the sources and targets in the four positions of either a lower-upper or a left-right connectron pair. A totally synthetic pair of dominant - anti-dominant connectrons could also be designed de-novo.

The connectron 5441 has a C1-T1 binding length of 82 bases and a C2-T2 binding length of 35 bases. The shorter of the two matches at 34 bases produces the lifetime for this connectron. The connectron 5500 has a C1-T1 binding length of 16 bases and a C2-T2 binding length of 16 bases. Either of the two matches at 16 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 9c is 544.

	genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
5	sequence of match									
10	yst	5441	3	3	2944 CP	84.112	84.193	l/u g		82
15	SEQ ID No. 249 ATACGTTTGAAGAAATCACTTTATGGATTGAAACAAAGTGGAGCGAACTG GTACGAACTATCAAATCATACCTGATAAAAC yst 5441 3 3 2901 TP 82.743 82.824 l/u g 82									
20	SEQ ID No. 250 ATACGTTTGAAGAAATCACTTTATGGATTGAAACAAAGTGGAGCGAACTG GTACGAACTATCAAATCATACCTGATAAAAC yst 5441 3 3 2965 CP 84.195 84.228 l/u g 34									
25	SEQ ID No. 251 GAAACGTGACGGTACTCATAAAGCTAGATTTGTT yst 5441 3 3 3529 TP 169.327 169.360 l/u g 34									
	SEQ ID No. 252 GAAACGTGACGGTACTCATAAAGCTAGATTTGTT									
30	yst	5500	3	3	3387 CN	151.534	151.549	l/u g		16
	SEQ ID No. 253 TAATTGTTGGGATTCC yst 5500 3 3 3526 TN 169.308 169.323 l/u g 16									
35	SEQ ID No. 254 TAATTGTTGGGATTCC yst 5500 3 3 3387 CN 151.516 151.531 l/u g 16									
	SEQ ID No. 255 AAAGGCTATAATATTA yst 5500 3 3 2905 TN 82.825 82.840 l/u g 16									
40	SEQ ID No. 256 AAAGGCTATAATATTA									

Found L/U DA AB - CD Connectron pair for 5441 and 5500 with a lifetime = 34 X 16 = 544



Design of an asymmetric lower-upper connectron pair in *H. sapiens*

There are many ways to design a pair of connectrons. In this example we have chosen to replace the C1 source and the T1

target of the right naturally occurring connectron with another sequence. Design of a connectron pair can be accomplished by anyone skilled the art by modifying and/or replacing any of the sources and targets in the four positions of either a lower-
 5 upper or a left-right connectron pair. A totally synthetic pair of anti-dominant - dominant connectrons could also be designed de-novo.

10 The connectron 395760 has a C1-T1 binding length of 32 bases and a C2-T2 binding length of 32 bases. Either of the two matches at 32 bases produces the lifetime for this connectron. The connectron 395762 has a C1-T1 binding length of 40 bases and a C2-T2 binding length of 39 bases. The shorter of the two
 15 matches at 39 bases produces the lifetime for this connectron. The lifetime of this pair of anti-dominant - dominant connectrons as shown in figure 10c is 1248.

genome	Connectron id	chromosome	contig	(.groups) id	match start	match stop	type of Connectron	source of Connectron	length of match
sequence of match				type					
hsd 395760 920		19 747775 CP 17572.332			17572.363	1/r g			32
<u>SEQ ID No. 257</u>		CCAGCCCCTCCTCCCTCAGACCCAGGAGTCCA							
hsd 395760 922		19 765474 TN 27988.178 27988.209			1/r g				32
<u>SEQ ID No. 258</u>		CCAGCCCCTCCTCCCTCAGACCCAGGAGTCCA							
hsd 395760 920		19 747777 CP 17572.369 17572.400			1/r g				32
<u>SEQ ID No. 259</u>		CCAGCCCCTCCTCCCTCAGACCCAGGAGTCCA							
hsd 395760 922		19 765567 TP 28004.852 28004.883			1/r g				32
<u>SEQ ID No. 260</u>		CCAGCCCCTCCTCCCTCAGACCCAGGAGTCCA							
hsd 395762 920		19 747819 CP 17573.447 17573.486			1/r g				40
<u>SEQ ID No. 261</u>		CCCCAGCCCCTCCTCCCTCAGACCCAGGAGTCCAGACCCC							
hsd 395762 922		19 765474 TN 27988.176 27988.215			1/r g				40
<u>SEQ ID No. 262</u>		CCCCAGCCCCTCCTCCCTCAGACCCAGGAGTCCAGACCCC							
hsd 395762 920		19 747823 CP 17573.520 17573.557			1/r g				39
<u>SEQ ID No. 263</u>		GGCCCCAGCCCCTCCTCCCTCAGACCCAGGAGTCCAGGT							
hsd 395762 922		19 765567 TP 28004.848 28004.887			1/r g				39
<u>SEQ ID No. 264</u>		GGCCCCAGCCCCTCCTCCCTCAGACCCAGGAGTCCAGGT							

Found L/R AD AB - CD Connectron pair for 395760 and 395762 with a lifetime = 32 X 39 = 1248

0.006 0.004

27988.178 27988.209 28004.852 28004.883 --- 27988.176 27988.215 28004.848 28004.887

